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RESULT 2
ABV30199 ID ABV30199 standard; cDNA; 4804 BP.
XX AC
XX ABV30199;
XX DT 16-SEP-2002 (first entry)
XX DE Human prostate expression marker cDNA 30190.
XX KW Human; prostate cancer; cytostatic; carcinogen; pharmacodynamic marker;
XX KW pharmacogenomic marker; gene; ss.
XX OS Homo sapiens.
XX MN WC020160860-A2.
XX PD 23-AUG-2001.
XX PF 20-FEB-2001; 2001WO-US05171.
XX PR 17-FEB-2000; 2000US-183139P.
XX PR 16-MAR-2000; 2000US-189662P.
XX PR 25-MAY-2000; 2000US-207454P.
XX PR 09-JUN-2000; 2000US-211314P.
XX PR 18-JUL-2000; 2000US-219007P.
XX PR 13-DEC-2000; 2000US-255281P.
XX PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
XX PI Schlegel R, Endege WO, Monahan JE;
XX DR WPI; 2001-662795/76.
XX PT Novel isolated nucleic acid molecule associated with cancerous state of
XX PT prostate cells and correlating with presence of prostate cancer, useful
XX PT for detecting presence of prostate cancer, stage of prostate cancer.
XX
XX Claim 1; Page 6542-6543; 11750pp; English.
XX
XX The invention relates to an isolated nucleic acid molecule (I) comprising
XX a nucleotide sequence given in Tables 1-9 (ABV00010-ABV62213) of the
XX specification or its complement. (I) is useful for:
XX (a) assessing whether a patient is afflicted with prostate cancer;
XX (b) monitoring the progression of prostate cancer in a patient;
XX (c) assessing the efficacy of a test compound to inhibit prostate
XX cancer in a patient;
XX (d) assessing the efficacy of a therapy for inhibiting prostate cancer
XX in a patient;
XX (e) selecting a composition for inhibiting prostate cancer in a patient;
XX (f) assessing the prostate cell carcinogenic potential of a compound;
XX (g) determining whether prostate cancer has metastasized in a patient;
XX (h) assessing the aggressiveness or indolence of prostate cancer in a
XX patient;
XX (I) is also useful as a pharmacodynamic or pharmacogenomic marker.
XX
SQ Sequence 4804 BP; 1605 A; 910 C; 1244 G; 1016 T; 29 other:
Query Match 99.3%; Score 4723.8; DB 23; Length 4804;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 4725; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1 GACGGCGGAGCCGCTGCTCCGGCTGAGGGAATAGAGACAGCTCCGCTCCTAGTGA 60
DB 49 GACGGCGGAGCGCGGTGCTCCCGCGCTGAGGGAATAGAGACAGCTCCGCTCCTAGTGA 108
QY 61 GCGCAGGGGAGCGAGAAGTATGACAGCGCAGAGTGGCTGTGAGTCACTCCTAGAAATCA 120
DB 109 GCGCAGGGGAGCGAGAAGTATGACAGCGCAGAGTGGCTGTGAGTCACTCCTAGAAATCA 168
QY 121 ATGACCAACAGCTATTTCACAGAGGAGACAGATAGTCTTACAGATAGTGCAGAGGCA 180

Db 169 ATGACCCAAACGTCATTTCACAGAGAGAGAGAGATGCTTCAGATGCTGACAGGCGCA 228
 Qy 181 GCTATGAAACATTTGAGACCCCTTGAGTGAAGAGAGATTCAGATGAGAGATATTTGAAGTA 240
 Db 229 GCTATGAAACATTTGAGACCCCTTGAGTGAAGAGAGATTCAGATGAGAGATATTTGAAGTA 288
 Qy 241 AGAAGTTGAAAGAGAGAGAGTCTCAAGAGAGATTCGAAACAGAGAGAGAGAGAGAGAG 300
 Db 289 AGAAGTTGAAAGAGAGAGAGTCTCAAGAGAGATTCGAAACAGAGAGAGAGAGAGAGAG 348
 Qy 301 CCTCTCCAGAGAGAGAGTCTCAAGAGAGATTCGAAACAGAGAGAGAGAGAGAGAGAG 360
 Db 349 CCTCTCCAGAGAGAGAGTCTCAAGAGAGATTCGAAACAGAGAGAGAGAGAGAGAGAG 408
 Qy 361 CTGGGAGAGAGAGAGAGTCTCAAGAGAGATTCGAAACAGAGAGAGAGAGAGAGAGAG 420
 Db 409 CTGGGAGAGAGAGAGAGTCTCAAGAGAGATTCGAAACAGAGAGAGAGAGAGAGAGAG 468
 Qy 421 ACATGAGAGAGAGAGAGTCTCAAGAGAGATTCGAAACAGAGAGAGAGAGAGAGAGAG 480
 Db 469 ACATGAGAGAGAGAGAGTCTCAAGAGAGATTCGAAACAGAGAGAGAGAGAGAGAGAG 528
 Qy 481 TGAGTCTTCAGTCTGAGAGAGTCTCAAGAGAGATTCGAAACAGAGAGAGAGAGAGAG 540
 Db 529 TGAGTCTTCAGTCTGAGAGAGTCTCAAGAGAGATTCGAAACAGAGAGAGAGAGAGAG 588
 Qy 541 ACATGAGAGAGAGAGAGTCTCAAGAGAGATTCGAAACAGAGAGAGAGAGAGAGAGAG 600
 Db 589 ACATGAGAGAGAGAGAGTCTCAAGAGAGATTCGAAACAGAGAGAGAGAGAGAGAGAG 648
 Qy 601 AGAAGAGAGAGAGAGAGAGTCTCAAGAGAGATTCGAAACAGAGAGAGAGAGAGAGAG 660
 Db 649 AGAAGAGAGAGAGAGAGAGTCTCAAGAGAGATTCGAAACAGAGAGAGAGAGAGAGAG 708
 Qy 661 AGAAGAGAGAGAGAGAGAGTCTCAAGAGAGATTCGAAACAGAGAGAGAGAGAGAGAG 720
 Db 709 AGAAGAGAGAGAGAGAGAGTCTCAAGAGAGATTCGAAACAGAGAGAGAGAGAGAGAG 768
 Qy 721 TTTTGAAGTCTGAGAGAGTCTCAAGAGAGATTCGAAACAGAGAGAGAGAGAGAGAG 780
 Db 769 TTTTGAAGTCTGAGAGAGTCTCAAGAGAGATTCGAAACAGAGAGAGAGAGAGAGAG 828
 Qy 781 AATGATGAGAGAGAGAGTCTCAAGAGAGATTCGAAACAGAGAGAGAGAGAGAGAGAG 840
 Db 829 AATGATGAGAGAGAGAGTCTCAAGAGAGATTCGAAACAGAGAGAGAGAGAGAGAGAG 888
 Qy 841 TGAGAGTGGGGTCCATTCATTTGAGAGAGAGAGTGTATCAAGAGAGAGAGAGAGAG 900
 Db 889 TGAGAGTGGGGTCCATTCATTTGAGAGAGAGAGTGTATCAAGAGAGAGAGAGAGAG 948
 Qy 901 AGAAGAGAGAGAGAGAGAGTCTCAAGAGAGATTCGAAACAGAGAGAGAGAGAGAGAG 960
 Db 949 AGAAGAGAGAGAGAGAGAGTCTCAAGAGAGATTCGAAACAGAGAGAGAGAGAGAGAG 1008
 Qy 961 AGCAGCTTATTCGAGAGTCTCAAGAGAGATTCGAAACAGAGAGAGAGAGAGAGAGAG 1020
 Db 1009 AGCAGCTTATTCGAGAGTCTCAAGAGAGATTCGAAACAGAGAGAGAGAGAGAGAGAG 1068
 Qy 1021 TTTGATGATTTCTTCAAGAGTCTCAAGAGAGATTCGAAACAGAGAGAGAGAGAGAGAG 1080
 Db 1069 TTTGATGATTTCTTCAAGAGTCTCAAGAGAGATTCGAAACAGAGAGAGAGAGAGAGAG 1128
 Qy 1081 TGAAGTATCTAAATATCAAGTCAAGAGAGATTCGAAACAGAGAGAGAGAGAGAGAGAG 1140
 Db 1129 TGAAGTATCTAAATATCAAGTCAAGAGAGATTCGAAACAGAGAGAGAGAGAGAGAGAG 1188
 Qy 1141 CTGAATGAGAGAGAGAGTCTCAAGAGAGATTCGAAACAGAGAGAGAGAGAGAGAGAG 1200
 Db 1189 CTGAATGAGAGAGAGAGTCTCAAGAGAGATTCGAAACAGAGAGAGAGAGAGAGAGAG 1248
 Qy 1201 AAGTGAAGAGAGAGAGTCTCAAGAGAGATTCGAAACAGAGAGAGAGAGAGAGAGAG 1260
 Db 1249 AAGTGAAGAGAGAGAGTCTCAAGAGAGATTCGAAACAGAGAGAGAGAGAGAGAGAG 1308

Qy 1261 ATGAGTCTTCAGAGAGAGATTTGGTAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1320
 Db 1309 ATGAGTCTTCAGAGAGAGATTTGGTAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1368
 Qy 1321 AGCAGAGTGCATTAACCTTCAAGTGGGAGAGAGTCTCAAGAGAGAGAGAGAGAGAGAG 1380
 Db 1369 AGCAGAGTGCATTAACCTTCAAGTGGGAGAGAGTCTCAAGAGAGAGAGAGAGAGAGAG 1428
 Qy 1381 TCCTGGGAGAGAGAGTCAAGTGAAGAGATTCAGAGAGAGAGAGAGAGAGAGAGAGAG 1440
 Db 1429 TCCTGGGAGAGAGAGTCAAGTGAAGAGATTCAGAGAGAGAGAGAGAGAGAGAGAGAG 1488
 Qy 1441 ATGAGTCTTCAG 1500
 Db 1489 ATGAGTCTTCAG 1548
 Qy 1501 CTGAG 1560
 Db 1549 CTGAG 1608
 Qy 1561 TGAGTATCTTAAG 1620
 Db 1609 TGAGTATCTTAAG 1668
 Qy 1621 AAGATTCCTTTGATGATCTTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1680
 Db 1669 AAGATTCCTTTGATGATCTTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1728
 Qy 1681 GTTCTGAG 1740
 Db 1729 GTTCTGAG 1788
 Qy 1741 ACGTATGAG 1800
 Db 1789 ACGTATGAG 1848
 Qy 1801 CTGAGTCTTAAG 1860
 Db 1849 CTGAGTCTTAAG 1908
 Qy 1861 TTTGAGTCTTAAG 1920
 Db 1909 TTTGAGTCTTAAG 1968
 Qy 1921 AGAAGCCCAAG 1980
 Db 1969 AGAAGCCCAAG 2028
 Qy 1981 AAG 2040
 Db 2029 AAG 2088
 Qy 2041 AGAAG 2100
 Db 2089 AGAAG 2148
 Qy 2101 ATCAG 2160
 Db 2149 ATCAG 2208
 Qy 2161 AAATGAGATTAAG 2220
 Db 2209 AAATGAGATTAAG 2268
 Qy 2221 CTGATCCAG 2280
 Db 2269 CTGATCCAG 2328
 Qy 2281 AAGTGGTCTACTCTCTCAAG 2340
 Db 2329 AAGTGGTCTACTCTCTCAAG 2388

	Best Local Similarity	54.3%	Prod No. 3e-111:	
	Matches 2085:	Conservative	0;	Mismatches 1523; Indels 231; Gaps 21;
QY	184	ATGAACAAATTTGACCCCTTGAGTGAAGAGATTCAGATSAAGATATTGTGAAGTAAGA	243	
QY	186	ATAAATTAATTTGGTTGTGTGGAGGATTAAGATACAGATGATGAATCTTGTTCTATAAA	245	
QY	244	AGTTGAAAAACGGAAGCTTCTACAAAGCAGTGA---TTCCCAAAACAGAGACACAAATG	300	
QY	246	AATCTAAAAAAGAGAAATTTGGTGGATATGTACAGTACAGACAAATTTGGAAAGCGCTA	305	
QY	301	CCCTCCGAGAAAACACTACCTATGACAGTCCGAGAGAGAAATATAAGAGATTTATATG	360	
QY	306	ATTTTGCAGATTAAGTAAAGGGCAGCTCTGTATATAGTGAAGATTTGGAGACTATGCTGTG	365	
QY	361	CTGGGAAAAATACAAAAATCAAAAGATTTTACAAAATCTGCGAGACAGTGTAAAGTT	420	
QY	366	CTTATAGAGA---AAAACCAAGAAAGATCCGTGACCTGATTTGGACAGTGCATTAAGT	422	
QY	421	ACATGAAAAGATCTTTGTATCAGAAAATCTTGAACGAGAGGAGAACTCTGTAGAGC	480	
QY	423	ATCATGAGCTGATGTTCAATAATGATCAAGTAAATATGACGTGAATACCTGAGTACG	482	
QY	481	TGAGCTTCAGCTCGAAACTGTACAGACCTTACACACTGACAGAAAGAGTTCCAAAAAGC	540	
QY	483	AACATGATAGCTGTGGAGAAAGGAAACTCATCTGTGAAGCTTAAACACAGCAAGTCTTGA	542	
QY	541	ACATCATGATGAAGAAAGAGCACTGCGAGAAACCAAAAGTAAATCAATAAAGACAGTG	600	
QY	543	AAATAACAACTGACACTAATTAAGAGAAATCTGTGAAGATTAATCAAGGCCCAATATTC	602	
QY	601	AGAAAGAGAGAGAAAAATGAAAAAAATTTAGACAGCTAAAAAAGAAAGAAACAAAAAAC	660	
QY	603	CGAAAGAAACATTTAAAGAGGAGCAAAACAGAAATCAAAAGA-----	646	
QY	661	AGGAAGAGATGTGAACACCCATTTAATACAGTGGCTCTCTCTGTGATTAAGAC	720	
QY	647	--GTTTGTGAAGCTGAGGCAATTTAATATACAGTGGCTTACTCCACAGATGGAGATC	704	
QY	721	TTTTTGAACATGGGTTGGAGATGAATAATACCTCCATGTGAAGATGAAGATCATATG	780	
QY	705	TTTTTGACAAATGGGGTGGAAAAATGAGTGAATCT---AATGAAGAAGAGATTTCTCTTG	761	
QY	781	AATCAATAGAGCGAGCTGTAAAAACAAATAAAAAGCACAAAGAAAAAGAACATCTT	840	
QY	762	AAGCATATCCGGGCAAAAATGAAAGCAAACT-----GAATATCTATTTCTGCTG	809	
QY	841	TGAGAGTGGGGGTCATCTATTTGAGAAAGAGTGAATCAAAAGAACACAGAGGA	900	
QY	810	AAATTTTGAAGACTTTGAACTTGATATCTAAGGCAATCAAGAAATCCCAAGAAAAAGAA	869	
QY	901	AGGAAGAAAGGACAGCCAGATTAAATGAAGAGCATTTAAACAACTGATAGTGAAGCTC	960	
QY	870	AGGAACGAAAGAGCTGGCGGACTTGTGTAAAGCCATGAACAAATGACAGTGAAGACC	929	
QY	961	AGCGGCTAATTCGAGAGCTGCACTGAACCTTCATATCATATATGCGGTGAATTAAGCA	1022	
QY	930	AAAGACTAATCGTGAATCTTCTATATCTTTACCAATCTCTTACTGTGAACCAAAACAA	989	
QY	1021	TTTCATGATTTCTTCAAAAGTAAACCCCGGGCCACTTGCACGAGAAATGCGATGCGCAT	1086	
QY	990	TCCATGATTTTTCAAAAGGCGTCCAAAGGCGCTCTTGTCTCAAGAAATGCAATGCACTTA	1044	
QY	1081	TGAAGTCTATTAATATACGTCAAGCCATACAAAGAAATCATATAGCACTGCATAATACTA	1144	
QY	1050	TAAAGTCAACAAATACAGCCCTGCACTAGAGAAAAAACCCTAATG-----	1100	
QY	1141	CTGAATGAACAGTATACCATAGTAAAGTTCTGAGCAGACAAAGGTGACAGAAATG	1200	
QY	1101	-----AGGAATATGTGCTGAAGTTCT	1122	
QY	1201	AAGTGAACATTAATGCACTCCCTGTAGTTTCAAGAAACCCAGATCAATTACTGATCAG	1266	